

GenCore version 4.5  
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## OM nucleic - nucleic search, using sw model.

Run on: September 17, 2002, 00:35:59 ; Search time 311.51 Seconds

(\*without alignments)  
9882.275 Million cell updates/sec

Title: US-09-719-017A-2  
Perfect score: 1793  
Sequence: 1 gaattccctgtgacaatta.....caattactcaatggcccg 1793

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 85457221 residues

Total number of hits satisfying chosen parameters:

3472872

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_032802:\*

1: /\$IDS1/gcdata/geneseq/geneseq/geneseq/geneseq -emb1/NA1980.DAT: \*  
2: /\$IDS1/gcdata/geneseq/geneseq/geneseq -emb1/NA1981.DAT: \*  
3: /\$IDS1/gcdata/geneseq/geneseq/geneseq -emb1/NA1982.DAT: \*  
4: /\$IDS1/gcdata/geneseq/geneseq/geneseq -emb1/NA1983.DAT: \*  
5: /\$IDS1/gcdata/geneseq/geneseq/geneseq -emb1/NA1984.DAT: \*  
6: /\$IDS1/gcdata/geneseq/geneseq -emb1/NA1985.DAT: \*  
7: /\$IDS1/gcdata/geneseq/geneseq -emb1/NA1986.DAT: \*  
8: /\$IDS1/gcdata/geneseq/geneseq -emb1/NA1987.DAT: \*  
9: /\$IDS1/gcdata/geneseq/geneseq -emb1/NA1988.DAT: \*  
10: /\$IDS1/gcdata/geneseq/geneseq -emb1/NA1989.DAT: \*  
11: /\$IDS1/gcdata/geneseq/geneseq -emb1/NA1990.DAT: \*  
12: /\$IDS1/gcdata/geneseq/geneseq -emb1/NA1991.DAT: \*  
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19: /\$IDS1/gcdata/geneseq/geneseq -emb1/NA1998.DAT: \*  
20: /\$IDS1/gcdata/geneseq/geneseq -emb1/NA1999.DAT: \*  
21: /\$IDS1/gcdata/geneseq/geneseq -emb1/NA2000.DAT: \*  
22: /\$IDS1/gcdata/geneseq/geneseq -emb1/NA2001.DAT: \*  
23: /\$IDS1/gcdata/geneseq/geneseq -emb1/NA2001B.DAT: \*  
24: /\$IDS1/gcdata/geneseq/geneseq -emb1/NA2002.DAT: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	DB ID	Description	RESULT	1
1	1793	100.0	1793	21 AAA47190	Nucleotide sequence	AAA47190	ID AAA47190 standard; DNA; 1793 BP.
2	1793	100.0	1793	21 AAZ4325	Nucleotide sequence	XX	AC AAA47190;
3	1126.4	62.8	1727	15 AAQ86279	Nitrolyase enzyme C	XX	DT 03-OCT-2000 (first entry)
4	954.2	53.2	1071	21 AAI2173	A. faecalis nitril	XX	DE Nucleotide sequence of the expression cassette of prPA-BCAT41.
5	404	22.5	5096	16 AAQ83824	Plasmid pKK222-8.	XX	KW Methionine: 2-hydroxy-4-methylthiobutanoic acid; nitrilase;
6	404	22.5	5110	16 AAQ83833	Plasmid PCM-64.	XX	KW nitrile hydratase; amidase; prPA-BCAT41; ss.
7	404	22.5	5110	16 AAQ83834	Plasmid PCM-P1208.	XX	KW
8	404	22.5	5110	16 AAQ83835	Plasmid pCM-P031.	XX	OS Synthetic.
9	22.5	5110	16 AAQ83836	Plasmid pCM-T221.	XX	PN WO200036120-A1.	
10	404	22.5	5110	16 AAQ83825	Plasmid PCM-X#.	XX	S
11	404	22.5	5110	16 AAQ83826	Plasmid PCAT10-1.	XX	
12	404	22.5	5110	16 AAQ83827	Plasmid PCM-T297.	XX	
13	404	22.5	5110	16 AAQ83828	Plasmid PCM-P1160.	XX	
14	404	22.5	5110	16 AAQ83829	Plasmid PCM-T270.	XX	
15	404	22.5	5110	16 AAQ83830	Plasmid PCM-P1198.	XX	
16	404	22.5	5110	16 AAQ83831	Plasmid PCM-T286.	XX	
17	404	22.5	5110	16 AAQ83832	rNB ribosomal RNA	XX	
18	403.6	22.5	502	16 AAQ9246	Telomerase coding	XX	
19	401.6	22.4	7688	20 AAX13349	Telomerase coding	XX	
20	401.6	22.4	7797	20 AAX13350	Telomerase coding	XX	
21	401.6	22.4	7797	20 AAX13350	Sequence of recomb	XX	
22	388.4	21.7	4222	10 AAN9038	Sequence of recom	XX	
23	388.4	21.7	4466	10 AAN90286	Plasmid PTP104.	XX	
24	388.4	21.7	4466	15 AAQ56337	PTP104 sequence.	XX	
25	386.8	21.6	4207	10 AAN9031	Sequence of recom	XX	
26	385.2	21.5	4204	12 AAO10279	Sequence of plasm	XX	
27	385.2	21.5	5641	22 AAF39800	Vector plasmid pJM	XX	
28	336	18.7	5670	22 AAF39801	Vector plasmid pJM	XX	
29	336	18.7	5826	22 AAF30798	Vector plasmid pDV	XX	
30	336	18.7	6071	22 AAF30799	Vector plasmid pDV	XX	
31	332.8	18.6	3753	24 ABA01129	Plasmid PHCE19T(II)	XX	
32	332.8	18.6	3755	24 ABA01130	Plasmid PSB-92 nuc	XX	
33	332.8	18.6	3950	22 AAF81854	Sequence of pl	XX	
34	332.8	18.6	4176	10 AAN90709	Human tissue facto	XX	
35	332.8	18.6	4214	21 AAA62632	Human tissue facto	XX	
36	332.8	18.6	4214	21 AAA6260	Nucleotide sequenc	XX	
37	332.8	18.6	4357	22 AAF33899	Expression vector	XX	
38	332.8	18.6	4816	22 AAD07799	PTCH1B vector co	XX	
39	332.8	18.6	5021	21 AAD07755	DNA sequence of pl	XX	
40	332.8	18.6	5027	20 AAX78865	Human tissue facto	XX	
41	332.8	18.6	5069	20 AAX78874	Human tissue facto	XX	
42	43	18.6	5069	20 AAX78871	Human tissue facto	XX	
43	332.8	18.6	5099	20 AAX78896	Human tissue facto	XX	
44	332.8	18.6	5104	22 AAD07798	PTK2HisB vector co	XX	
45	332.8	18.6	5132	20 AAX78883	Human tissue facto	XX	

## ALIGNMENTS

RESULT

1

AAA47190

ID AAA47190 standard; DNA; 1793 BP.

XX

AC AAA47190;

XX

DT 03-OCT-2000 (first entry)

XX

DE Nucleotide sequence of the expression cassette of prPA-BCAT41.

XX

KW Methionine: 2-hydroxy-4-methylthiobutanoic acid; nitrilase;

KW nitrile hydratase; amidase; prPA-BCAT41; ss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT CDS 123..1193

FT FT /\*tag= a















XX	Plasmid pCM-X#; bacteriophage T7; RNA polymerase; mutant promoters; circular; cyclic; ds.	KW	RESULT 11
OS	Synthetic.	XX	AAQ83826
XX	Key Promoter 198..220	FT	ID AAQ83826 standard; DNA; 5110 BP.
XX	/*tag= a	FT	AC AAQ83826;
XX	/note= "potential T7 promoter prior to a promoterless chloramphicol acetyl transferase gene"	FT	XX 04-OCT-1995 (first entry)
XX	US5385834-A.	PR	DE Plasmid pCAT10-1.
XX	31-JAN-1995.	PD	XX
XX	13-AUG-1993; 93US-0106433.	PF	OS Synthetic.
XX	(GBOR-) GEORGIA TECH RES CORP.	PA	XX
XX	Ikeda RA;	PI	XX
XX	DR WPI; 1995-081565/11.	DR	XX
XX	New mutant form of T7 RNA polymerase - able to utilise a wide range of T7 promoter sequences having mutations that inactivate recognition by wild type enzyme	PT	XX
XX	PS Disclosure; Columns 43-50; 79pp; English.	PT	XX
XX	AAQ83825 is the plasmid pCM-X#, it was used in the production of claimed bacteriophage T7 RNA polymerase mutant promoters.	CC	XX
XX	Sequence 5110 BP; 1303 A; 1287 C; 1288 G; 1226 T; 6 other;	SQ	XX
XX	Query Match 22.5%; Score 404; DB 16; Length 5110; Best Local Similarity 96.5%; Pred. No. 4.9e-78; Matches 413; Conservative 0; Mismatches 15; Indels 0; Gaps 0;	XX	XX
Qy	1257 aggtcgaccgtggaggcttgcgaactttgggtccacatccatgcgaactcagaag 1326	Qy	XX
Db	1251 aggttgcgtggcgacatggcgatggcgaaactcagaag 1310	Db	XX
Qy	1327 tgaacacggcgtaacgcctataggtagtggtgggtcccatgcgagatggaaactggcc 1386	Qy	XX
Db	1311 tgaacacggcgtaacgcctatgggtgggtcccatgcgagatggaaactggcc 1370	Db	XX
Qy	1387 aggcatcaataaacggaaaggcgttgcgaagactgggccttcgtttatctgtgt 1446	Qy	XX
Db	1371 aggcatcaataaacggaaaggcgttgcgaagactgggccttcgtttatctgtgt 1430	Db	XX
Qy	1447 ttgcggggaaacctcttcgttgcgttgcgttgcgtttatctgtgt 1505	Qy	XX
Db	1431 ttgcggggaaacctcttcgttgcgttgcgttgcgtttatctgtgt 1490	Db	XX
Qy	1507 aaccaacggccggagggtggcgccggcggccataactgcggcatcaatt 1566	Qy	XX
Db	1491 aaccaacggccggagggtggcgccggccataactgcggcatcaatt 1550	Db	XX
Qy	1567 aaccaacggccggagggtggcgccggccataactgcggcatcaatt 1626	Qy	XX
Db	1551 aaccaacggccggagggtggcgccggccataactgcggcatcaatt 1610	Db	XX
Qy	1627 attcctacaacggcatccccccacatggtaactacttcgttttcgttgcgt 1686	Qy	XX
Db	1611 attcctacaacggcatccccccacatggtaactacttcgttttcgttgcgt 1670	Db	XX
Qy	1687 gggctat 1694	Qy	XX
Db	1671 qcqctqt 1678	Db	XX

Qy 1567 aacgagaaggccatccgtacggatggcttttgcgttctacaactcttctcgatc 1626  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1551 aacgagaaggccatccgtacggatggcttttgcgttctacaactcttctcgatc 1610  
 Qy 1627 atatctaacaaggcatccccacagatacggtaactagctcggtttgatcggaa 1686  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1611 atatctaacaaggcatccccacagatacggtaactagctcggtttgatcggaa 1670  
 Qy 1687 gcaatgt 1694  
 |||||  
 Db 1671 gcaatgt 1678

RESULT 12  
 AAQ83827 ID AAQ83827 standard; DNA; 5110 BP.

AC AAQ83827;  
 XX  
 04-OCT-1995 (first entry)  
 DE Plasmid PCM-T297.  
 XX  
 KW plasmid PCM-T297; bacteriophage T7; RNA polymerase;  
 KW mutant -11G to T; T7 promoter phi 10; circular; cyclic; ds.  
 KW  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT promoter 198..220  
 FT /\*tag= a  
 FT /note= "inactive T7 promoter phi 10 mutant (-11G to  
 T) Prior to a promoterless chloramphicol  
 acetyl transferase gene"  
 XX  
 US5385834-A.  
 PD 31-JAN-1995.  
 XX  
 PF 13-AUG-1993; 93US-0106433.  
 PR 13-AUG-1993; 93US-0106433.  
 PN (GEOR-) GEORGIA TECH RES CORP.  
 PR  
 XX  
 PI Ikeda Ra;  
 XX  
 DR WPI; 1995-081565/11.  
 XX  
 PT New mutant form of T7 RNA polymerase - able to utilise a wide  
 PT range of T7 promoter sequences having mutations that inactivate  
 PT recognition by wild type enzyme  
 XX  
 Disclosure: Columns 57-62; 79pp; English.  
 XX  
 CC AAQ83827 is the plasmid PCM-T297, it was used in the production of  
 CC the bacteriophage T7 RNA polymerase mutant promoter phi 10 -11G  
 CC to T substitution (claimed).  
 XX  
 SQ Sequence 5110 BP; 1305 A; 1288 C; 1288 G; 1229 T; 0 other;

Query Match 22.5%; Score 404; DB 16; Length 5110;  
 Best Local Similarity 96.5%; Pred. No. 4; ge-78; Matches 413; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1267 agatcgaccatccaggatgtacggatgtggccactgtacccatggactcaag 1326  
 ||||| ||||| |||||  
 Db 1251 aagatgttcgtccgtggccgtatggccgtggccactgtacccatggactcaag 1310  
 Qy 1327 tggaaacccgtatggccgtatgttgggttccatgtggactgtggaaatggcc 1386  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1311 tggaaacccgtatggccgtatgttgggttccatgtggactgtggaaatggcc 1370

RESULT 13  
 AAQ83828 ID AAQ83828 standard; DNA; 5110 BP.

AC AAQ83828;  
 XX  
 04-OCT-1995 (first entry)  
 DE Plasmid PCM-P1160.  
 XX  
 KW plasmid PCM-P1160; bacteriophage T7; RNA polymerase;  
 KW mutant -9G to G; T7 promoter phi 10; circular; cyclic; ds.  
 KW  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT promoter 198..220  
 FT /\*tag= a  
 FT /note= "inactive T7 promoter phi 10 mutant (-9G to  
 G) Prior to a promoterless chloramphicol  
 acetyl transferase gene"  
 XX  
 US5385834-A.  
 PN  
 PD 31-JAN-1995.  
 XX  
 PF 13-AUG-1993; 93US-0106433.  
 PR 13-AUG-1993; 93US-0106433.  
 PA (GEOR-) GEORGIA TECH RES CORP.  
 XX  
 PI Ikeda Ra;  
 XX  
 DR WPI; 1995-081565/11.  
 XX  
 PT New mutant form of T7 RNA polymerase - able to utilise a wide  
 PT range of T7 promoter sequences having mutations that inactivate  
 PT recognition by wild type enzyme  
 XX  
 Disclosure: Columns 63-70; 79pp; English.  
 XX  
 CC AAQ83828 is the plasmid PCM-P1160, it was used in the production of  
 CC the bacteriophage T7 RNA polymerase mutant promoter phi 10 -9G  
 CC to G substitution (claimed).  
 XX  
 Sequence 5110 BP; 1300 A; 1291 C; 1293 G; 1226 T; 0 other;



